

BLASTP 2.2.20+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: YSXAP003016

Database: NCBI Protein Reference Sequences  
5,790,914 sequences; 2,058,125,444 total letters

Query=  
Length=16

**No significant similarity found.** For reasons why, [click here](#).

Database: NCBI Protein Reference Sequences  
Posted date: Apr 17, 2009 6:11 PM  
Number of letters in database: 25,257  
Number of sequences in database: 331

Lambda	K	H
0.335	0.297	1.50

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Sequences: 331

Number of Hits to DB: 1834

Number of extensions: 110

Number of successful extensions: 110

Number of sequences better than 200000: 64

Number of HSP's better than 200000 without gapping: 0

Number of HSP's gapped: 92

Number of HSP's successfully gapped: 81

Length of query: 16

Length of database: 25257

Length adjustment: 6

Effective length of query: 10

Effective length of database: 23271

Effective search space: 232710

Effective search space used: 232710

T: 11

A: 40

X1: 1 (0.5 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 1 (3.6 bits)

S2: 0 (3.2 bits)